Exhibit B



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PROSITE: PDOC00885 (documentation)

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The following bacterial proteins, which seems to belong to a family of pseudouridine synthases (EC $\underline{4.2.1.70}$) [1] have been shown to share regions of similarities:

- Escherichia coli and Haemophilus influenzae 16S pseudouridylate 516 synthase (EC 4.2.1.70) (gene: rsuA). This enzyme is responsible for the formation of pseudouridine from uracil-516 in 16S ribosomal RNA.
- Escherichia coli hypothetical protein yciL and HI1199, the corresponding Haemophilus influenzae protein.
- Escherichia coli hypothetical protein yjbC.
- Escherichia coli hypothetical protein ymfC and HI0694, the corresponding Haemophilus influenzae protein.
- Aquifex aeolicus hypothetical protein AQ_554.
- Aquifex aeolicus hypothetical protein AQ_1464.
- Bacillus subtilis hypothetical protein ypuL.
- Bacillus subtilis hypothetical protein ytzF.
- Borrelia burgdorferi hypothetical protein BB0129.
- Helicobacter pylori hypothetical protein HP1459.
- Synechocystis strain PCC 6803 hypothetical protein slr0361.
- Synechocystis strain PCC 6803 hypothetical protein slr0612.

These are proteins of from 25 to 40 Kd which contain a number of conserved regions in their central section. They can be picked up in the database by the following highly conserved pattern.

- -Consensus pattern: G-R-L-D-x(2)-[STA]-x-G-[LIVFA]-[LIVMF](3)-[ST]-[DNST]
- -Sequences known to belong to this class detected by the pattern: ALL.
- -Other sequence(s) detected in SWISS-PROT: NONE.
- -Last update: July 1999 / Pattern and text revised.
- [1] Wrzesinski J., Bakin A., Nurse K., Lane B.G., Ofengand J. Biochemistry 34:8904-8913(1995).

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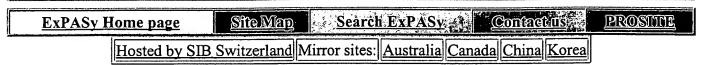


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PROSITE: PS01149

```
ID
     PSI RSU; PATTERN.
     PS01149;
AC
     NOV-1995 (CREATED); JUL-1999 (DATA UPDATE); JUL-1999 (INFO UPDATE).
DT
     Rsu family of pseudouridine synthase signature.
DE
     G-R-L-D-x(2) - [STA]-x-G-[LIVFA] - [LIVMF](3) - [ST] - [DNST].
PA
NR
     /RELEASE=38,80000;
     /TOTAL=18(18); /POSITIVE=18(18); /UNKNOWN=0(0); /FALSE POS=0(0);
NR
     /FALSE NEG=0; /PARTIAL=0;
NR
     /TAXO-RANGE=???P?; /MAX-REPEAT=1;
CC
     P35159, RLUB BACSU, T; P33918, RSUA ECOLI, T; P45124, RSUA HAEIN, T;
DR
DR
     051155, Y129_BORBU, T; 055578, Y361_SYNY3, T; 066829, Y554_AQUAE, T;
     P72581, Y612_SYNY3, T; P42395, YCIL_BUCAP, T; P37765, YCIL_ECOLI, T;
DR
     P45104, YCIL_HAEIN, T; P55986, YE59_HELPY, T; O67444, YE64_AQUAE, T;
DR
     P32684, YJBC ECOLI, T; P75966, YMFC ECOLI, T; P44827, YMFC HAEIN, T;
DR
     005668, YRSU_MYCLE, T; 033210, YRSU_MYCTU, T; 032068, YTZF_BACSU, T;
DR
DO
     PDOC00885;
//
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NiceSite - a user-friendly view of this PROSITE entry

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